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 Listing first 45 summaries
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te of mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
Class: transposon-tarrord
                                                                                                                                                                                                                                                        Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M. Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
                                                                                                                                                                                                                                                                                                                   AQ874584
AQ874584.1 GI:6286828
GSS.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                   P.O. Box 208103,
Tel: 203 432 9949
Fax: 203 432 6161
                                                                                                                                                                                                                                         Gene Disruption Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                         AQ874584 1ine V111B3 mTn-3xHA/lacZ Insertion Library, strain Cerevisiae genomic 5', genomic survey sequence.
                                                                                                                                                                                                                       Contact: Kumar Michael Snyder,
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Ross-Macdonald, P., Roemer, T.,
                                                                                                                                                                                                                Yale University
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Location/Qualifiers
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                        /clome lib="mTm-3xHA/lacZ Insertion Library strain Y2278"
/note="vector: pHSS6-Sa1; A yeast genomic DNA library
without 2 micron or mitochondrial DNA was prepared in
pHSS6-Sa1; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mTm-3xHA/lacZ
minitransposon containing lacZ, URA3, and tet resistance.
                     minitransposon
                                                                                   /organism="Saccharomyces cerevisiae"
/mol type="genomic DNA"
/strain="Y2278 - S288C background, c
/db xref="taxon:4932"
/lab host="E. coli"
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CC752307
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CC192318 CH257R04H2
B195766 LEZTR04H2
B19521 T907-T TAM
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CL510366 SAIL 829
AL064465 Drosophi1
AM633159 b104d09 x
AQ383493 RPCII1-15
CE806390 tigr-gss-
AG435289 Mus muscu
AM13335 se17e08.9
AG45267962 Pan trogl
BZ312600 id27a07.9
BZ327427 id27a07.9
BZ327427 id27a07.9
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AG458167 MUS muscu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                          Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefigenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen years species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bon,E., Neuveglise,C., Casaregola,S., Artiguenave,F., Aigle,M. and Durrens,P. Genomic exploration of the hemiascomycetous yeasts: 5. Saccharomyces bayanus var. uvarum FEBS Lett. 487 (1), 37-41 (2000)
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AL398217 AL398217.1 GI:12151528 GSS.
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1 (bases 1 to 927)
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                                                   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                Drosophila melanogaster genome
BACR19021 of RPCI-98 library f:
fly), genomic survey sequence.
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Genoscope.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTACAGTCTCGATAAT-AGAATAATAAGCGCGATTTTTGCTAGCGCCGCCGCCGC-----
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strong similarity to YKR076w and YGR154c ]"
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/note="end : T3"
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/db_xref="taxon:4931"
/clone="ASOAA007G06"
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/strain="CLIB 533"
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                                                                                                                                                                                                                 821 bp DNA linear GSS 03-JUN-1999 ter genome survey sequence TET3 end of BAC # library from Drosophila melanogaster (fruit
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Pred. No. 6.7e-29;
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.f: - Web : www.genoscope.cns.fr)

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JOURNAL COMMENT
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                                                                                                                                                                              AUTHORS
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                                                                                                 genomic survey sequence.

NC252581.1 GI:30589331
CC252581.1 GI:30589331
GSS.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
E 1 (bases 1 to 1055)
Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
Warren, W., Graves, T., Mardis, E. and Wilson, R.
Gallus gallus BAC End Reads
L Unpublished (2003)
L Contatt Bid Ard V Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clomes, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441
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                                                                                                                                                                                                                                                                                                                                                                                                                      CC252581 1055 bp
CH261-136H21_Sp6.1 CH261 Gallus
                Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
                                                                                     Contact: Richard K. Wilson
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/db_xref="taxon:7227"
/clone="BACR19021"
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Pred. No.
Std Error: 0.00
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) gallus
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GSS.
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                                                                                                                                                                                                                                        Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: Sp6 ATTTAGGTGACACTATAGCLass: BAC ends
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                                                                                                                                                                                                                     Genevieve Payan.
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/clone lib="CH261"
/clone lib="CH261"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"
                                                                                     /organism="Drosophila melanogaster'
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-136H21"
                    /clone_lib="DrosBAC"
/plasmīd="pBeloBAC11"
                                                                 clone="BACN37F10"
                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                 - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) this://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence SP6 end of BAC PACNO8K14 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                        pBeloBAC11
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                                               AATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTTTATTGCAGAGGACTAT 676
                                                                                 AVYAWRGGGGAATSGMGGAYCKGWAWTTTTYWWAWTWTTTTTTWWTTTKGWAAGMAAMSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAAAAAAAAAAGACTAATAATA 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGTTTCTGGGACGTCTTAACTTTTATTGCAGAGGACTATCAAATCATACAGATATTGT 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCTAGCTGGGAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTG
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              AACTATGGDTAAMTTTAWWAATTTTHTAAAGGGAAGAWTTWTTTTTTTAAGKGGCCTWT
                                                                                                                  AGCAAGCGGAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAATCATATAAAAGGGAGA 616
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                            /clone lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
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                                               255 TGTTTATTACATATGAAATTTCGATATTATTCCTTTTGGAAGGATAATTTTTGTGGGATAAA 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
Library was constructed by R. Haywood. DNA sequencing by:
Library was constructed by R. Haywood. DNA sequencing by:
Washington University Genome Sequencing Center For information on
Obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
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Plasmodium falciparum 3D7
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 436)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU Plasmodium EST Project
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                                                                                                                                                                          /note="Wector: pBluescript SK plus; Site_1: EcoRI; Site_2: XhoI; The library was constructed by R Haywood. cDNAs were synthesized from ganetocyte poly(A)+ RNA by oligo d(T) priming, size-selected and directionally cloned into the EcoRi (5' end) to XhoI (3' end) sites of the Uni-ZAP XR lambda vector (Stratagene). The primary library was mass excised as phagemid using the ExAssist helper phage (Stratagene). Clones were mass excised using the ExAssist helper phage (Stratagene), the phagemids were precitptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DHIOB cells. Clone Availability: David Sibley, Washington University."
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/lab_host="DH10B (GeneHog, Invitrogen,
/clone__ib="Plasmodium falciparum 3D7)
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Score 41.4; DI
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN03G04 of DrosBAC library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                        WKTDTDTWGKADTDWWTDTWKTTWTWTTTTTGWKKWDTKTKTKWKDDDGTTWTDTWKDW
                                                                               CTATCAAATCATACAGATATTGTCAAAAAAAAAAAAAAGACTAATAATAACAT 723
                                                                                                                  KDWDWKDADTKAGRKRGWGWKKKGGWKKTTKTKKKKKTDKTKTGTDTKWGWKDKWTDKKRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db xref.="taxon:7227"
/clone="BACN03604"
/clone | "bb="DrosBAC"
/plasmīd="pBeloBAC11"
/note="end : SP6"
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BH572702
BOGTD44TF BOGT Brassica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, J (E-mail:hattori@sc.riken.jp, URL:http://hgp.gsc.riken.go.jp/Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
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Submitted (17-NOV-2003) Massahira Hattori, The Institute of Physical
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LIBRARY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Sequences of Library MSMg01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus molossinus"
|mol type="genomic DNA"
|sub specise="molossinus"
|db_xref="taxon:57486"_____
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue type="mixture of kidney and spleen"/clone_Tib="MSMg01 Mouse Male BAC Library"
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/sex="male"
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                          Contact: Robert Strausberg, Ph
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                   1 (bases 1 to 791)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                    EST.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 698)

1 (bases 1 to 698)

1 (bases 1, Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)

Other GSSs: BOGTD44TR
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                 BI255759.1
                                                                                                                                                                                                                            mRNA sequence.
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                                                                                                                                                                    Homo sapiens (human)
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Fax: 301-838-0208
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Library Preparation: Life Technologies, Library Arrayed by: Incyte Genomics, In
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/clone_lib="BOGT"
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/strain="TO1000DH3"
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cDNA clone IMAGE:5122410
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High quality sequence stop: 711.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5122410"
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Pred. No. 3
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AL214492.1 GI:7873311
GSS; genome survey sequence.
GSS; genome nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                              Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J. Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
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lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Rutger S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 1485
Tel: 607 255 7886
Fax: 607 255 6683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366 bp mRNA linear EST CC-esflcLEL23G13d1 Tomato flower library from a mixture developmental stages Lycopersicon esculentum cDNA clone CC-esflcLEL23G13d1, mRNA sequence.
                                                                                                                                                                                                                                                                     ESTs from a tomato flower library
Unpublished (2001)
Contact: Rutger S. van der Hoeven
                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Solanaceae; Solanum; Lycopersicon.
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   van der Hoeven,R.S. and Tanksley,S.D.
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Lycopersicon esculentum
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Direct Submission
                                                                                                                                                                                             Email: rv19@cornell.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                         BG628729.1 GI:13680202
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ilarity 45.4%;
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 developmental stages"
                                                                                                     organism="Lycopersicon esculentum"
|mol_type="mRNA"
|cultivar="E6203"
              /tissue_type="developing flower buds
/dev_stage="4-8 week old plants"
/lab host="XLOLR"
/clone_lib="Tomato flower library fro
                                                                         /db_xref="taxon:4081"
/clone="cC-esflcLEL23G13d1"
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/clone="167C22"
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388 TCTGAATTGTTAGGTAGGGAAAGAGAGTTGATTCATTCGTGGTGCATCCAAAATGGTTGT
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Unpublished (1997)
Contact: Takuji Sasaki
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
National Institute of Program, Kannondai 2-1-2,
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 518)
Yamamoto, K. and Sasaki, T.
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EST.
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TGGGAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTC
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nilarity 57.0%;
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                                                                                                                                                                                                                               /dev_stage="ETiolated shoot (8 days
/clone_lib="Rice shoot"
/note="Etiolated shoot (8 days old)"
                                                                                                                                                                                                                                                                                        /cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="S5033_8Z"
                                                                                                                                                                                                                                                                                                                                         organism="Oryza sativa
/mol_type="mRNA"
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Search completed: August 27,
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AZ541311
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
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1 (bases 1 to 845)

Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HM1: MSS sheared DNA library
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High quality sequence stop: 612.
Location/Qualifiers
1. .845
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Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13-Reverse Class: shotgun
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Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: bjloftus@tigr.org
Clones are derived from the
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/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="HM1:IMSS"
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Pred. No. 4.8;
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1: geneseqn1980s:*
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ADA71938
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8060.213 Million cell updates/sec
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Aad07475 Yeast pro
Aad07497 pYMR251Ap
Aad07493 Yeast YMR
Aad07503 Yeast YMR
Abd76446 S. cerevi
Ada71938 Rice gene
Abs51325 CDNA enco
Adf96256 Colon can
Aas23224 Genomic s
Aba16123 Human ner
Abs63864 Human CDN
Abv04394 Human pro
Aal15477 Human mus
Abx58465 CDNA enco
Ad125192 Human mus
Abx36811 Bovine ES
Abq5918 Human col
Ads41207 Human aut
Acm58226 Cotton gy
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35.2	35.2	35.2	35.2	35.2	35.2	35.4	35.4	35.4	35.6	35.6	35.6	35.6	35.6	35.6	35.8	35.8	35.8	35.8	35.8	35.8	35.8	36	36.2	36.4
4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	5.0	5.0	5.0	5.0	5.0	5.0	5. O	5.0	5.0	5.0
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ADQ97316	ADS89390	ACN88712	ADA71938	AAZ41383	ABV96856	ACA64924	AAK70003	ABV18166	ACN37231	ADI82483	ADH29006	ABK09744	ABL58962	ACH17729	ADS89438	ACA40062	ADA56114	ACC50510	ADA39926	AAZ00806	ACN62578	ABL34113	ABT22885	ADS36499
Adq97316 Mouse can	Ads89390 Oligonucl	Acn88712 Breast ca	Ada71938 Rice gene	Aaz41383 Human nor	Abv96856 Human pan	Aca64924 Human PLZ	Aak70003 Human imm	Abv18166 Human pro	Acn37231 Human per	Adi82483 Human mod	Adh29006 Human chr	Abk09744 Human ova	Ab158962 Human tum	Ach17729 Human adu	Ads89438 Oligonucl	Aca40062 Prokaryot	Ada56114 Gene enco	Acc50510 Human sec	Ada39926 Human sec	Aaz00806 Human sec	Acn62578 Cotton de	Abl34113 Human imm	Abt22885 Breast ca	Ads36499 Human aut

ALIGNMENTS

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RESULT 1
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The invention relates to yeast promoters that are used to control the expression of homologous and heterologous sucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as ethanol or both. Therefore expression of nucleic acid molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters

New promoter sequences from Saccharomyces cerevisiae useful for controlling expression of homologous and heterologous nucleic ac expression in yeast cells.

acid

Claim 1; Page 67-68; 191pp; English.

WPI;

2001-367697/38.

Belfield G, Oakley C;

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RESULT 2
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AC AADO
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DT 10-A
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Best Local Similarity
Matches 723; Conser
           PYMR251AP DNA plasmid
                                 10-AUG-2001
                                                                         AAD07497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are useful for, inter alia, the high level production of proteins opolypeptides in yeast cell culture. The present DNA sequence is Saccharomyces cerevisiae YMRZ51WA promoter related to the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTATTCCTATCCCGTTGAAGCAACC
                                                                         standard;
                                                                                                                                                                                TCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTT
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                                                                                                                                                                                                                                                      TTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAA
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Pred. No. 9.2e-211;
Mismatches 0;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           Sequence 11427 BP; 3131 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 133-143; 191pp;
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GTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCGGGGCGCCCGTTTCCCA
                                                                                      GGGGGCTAAGAAGTCATTCACTTTCCTTTCCCCTTCGGGGTCCGGACCCGGGACCCCTCCT
                                                  GGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACA
                                                                                                                           CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATCCCGTTGAAGCAACC
                                                                                                                                                                                                    ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT
                                                                                                                                                                                                                                            CTTTCGATTAGCACGCACACACATCACATAGACTGCGTCATAAAAATACACTACGGAAAA
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                                                                                                                                                                                                                                                                                   100.0%;
llarity 100.0%;
Conservative C
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                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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Yeast; promoter; gene expression; fermentable carbon source; glucose; non-fermentable carbon source; ethanol; yeast cell culture;

Saccharomyces cerevisiae useful for smologous and heterologous nucleic

The invention relates to yeast promoters that are used to control the expression of homologous and heterologous nucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as glucose or a non-fermentable carbon molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters are useful for, inter alia, the high level production of proteins or polypeptides in yeast cell culture. The present sequence is pYMR251AP plasmid related to the invention: This plasmid contains pPRB1 and yeast

2589 C; 2527 G; 3180 Ŧ; 0 U; 0 Other;

Score 723; DB 4; Pred. No. 3.3e-210; Mismatches 0; Length 11427; Indels 0

180

74

254 240 194

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RESULT 3
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The invention relates to yeast promoters that are used to control the expression of homologous and heterologous nucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as glucose or a non-fermentable carbon molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae. Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast; promoter; gene expression; fermentable carbon source; glucose; non-fermentable carbon source; ethanol; yeast cell culture; pyMRZ51AP plasmid; luciferase gene; ds.
                                                                                                                                                                                                                                                            New promoter sequences from Saccharon controlling expression of homologous expression in yeast cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pYMR251AP+luc sequence DNA construct
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                                                       TTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAA
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                                                                                                                                               TTTCGATGAGAGAATTAGCAAGCGGAAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAA
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Yeast

YMR251WA promoter region

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                                                                                                                                                       Query Match
Best Local
                                                                                                             Matches
                                                                                                                                                                                 The invention relates to yeast promoters that are used to control the expression of homologous and heterologous nucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as glucose or a non-fermentable carbon molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters are useful for, inter alia, the high level production of proteins or polypeptides in yeast cell culture. The present DNA sequence is saccharomyces cerevisiae YMR251WA promoter region related to the
                                                                                                                                                                                                                                                                                                                                        New promoter sequences from Saccharomyces cerevisiae useful for controlling expression of homologous and heterologous nucleic acid expression in yeast cells.
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                                                                              CTTTCGATTAGCACGCACACACATCACATAGACTGCGTCATAAAAATACACTACGGAAAA
   GGGGGCTAAGAAGTCACTTTCTTTTTCCCTTCGCGGTCCGGACCCGGGACCCCTCCT
                                                                CTTTCGATTAGCACGCACACACACACACATAGACTGCGTCATAAAAATACACTACGGAAAA
                                                                                                             Conservative
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                                                                                                                      99.6%;
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                                                                                                           Score 720.4; DB 4;
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04-JAN-2001;
09-JAN-2001;
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                                                                                           21-DEC-2001;
                                                                                                                     22-AUG-2002
                                                                                                                                                                      Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                             cerevisiae BAX-associated cDNA fragment SEQ ID 317.
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                                                                                                                                                                                                                                                                                                                  ABQ76446;
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; 2001EP-00870003.
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(JANC) JANSSEN PHARM NV

Contreras

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Reekmans

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CC This invention describes a novel nucleic acid representing a synthetic companies. The Bax gene of the invention is useful for identifying Bax-cc resistant yeast or fungi, identifying, or obtaining and identifying CC Candida spp. sequences that are differentially expressed in a pathway community leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax-induced cell death or identifying inhibitors or commention have cytostatic, fungicide; immunosuppressive, virucide and compositions, compositions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 680 BP; 180 A; 142 C; 166 G; 192 T; 0 U; 0 Other;
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AAAAAGACTAATAATAACA 722
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                                                                                                                      TGGGACGTCTTAACTTTTATTGCAGAGGACTATCAAATCATACAGATATTGTCAAAAAAA
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Pred. No. 1.3e-141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chang H,
Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA71938 standard; DNA; 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                illustrate the invention.
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364
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                                                                                                                                                                                                                                                                                                CATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCGGGACCCCTCCTCCTCCCCGCACGATT 194
                                                                                                                                                                                                                                                                                                                                                            AKYKSGSMSKRMMMSSCGRSGCGRRSAYSRYYGTSRKYGTYKKMTYYSASRCMRAYMTTS
                                                                                                                                                                                                                                                                                                                                                                                                                       AGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGGATGGGGGCTAAGAAGT 134
                                                                                                                                                                            TCTTCCTTTCATATCTTCCTTTATTCCTATCCCGTTGAAGCAACCGCACTATGACTAAA
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WRMWRMTRRRWAKKSSRTSRRKKRKWCMRKRKYKRMRGYSRMRSCKRARWMKRCRSGRA
                                                        TGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTATCTCACAGTGGTAACGGCACCGT
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F, Quan
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S, Tao Y,
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(ie Z, Zhu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bursitis; cirrhosis; hepatitis; polycythaemia vera; anaemia; psoriasis; primary thrombocytopenia; cancer; adenocarcinoma; leukaemia; myeloma; sarcoma; immune system disorder; acquired immundedficiency syndrome; AIDS; allergy; asthma; Crohn's disease; diabetes mellitus; gout;
                                                                                                                                                                                                                                                                                                                                               16-JAN-2001;
17-JAN-2001;
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16-JAN-2001;
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Best Loc Matches Query Match

80;

Local

Similarity

5.3%;

Score 38.6; DB Pred. No. 0.94;

DB 6; 69;

Length Indels

Mismatches

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CC polypeptides (SPTM) and polymucleotides are useful in the diagnosis, and control study, prevention or treatment of diseases associated with decreased cc expression of functional SPTM, e.g. actinic keratosis, arteriosclerosis, ctribosis, hepatitis, polycythaemia vera, primary ctromoscytopenia, anaemia, psoriasis, cancers including adenocarcinoma, cleukaemia, myeloma or sarcoma, immune syent disorder such as acquired immunodeficiency syndrome (ADIS), allergies, asthma, Crohn's disease, cd diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, cc diabetes mellitus, hepatitis, multiple sclerosis, osteoporosis, cantratisis, neurological disorders such as epilepsy, stroke, Alzheimer's cd disease, pick's disease, Huntington's disease, dementia, parkinson's disease, pick's disease, Huntington's disease, dementia, parkinson's cd disease, other developmental disorder of the central nervous system, cmental disorder including mood, amxiety or schizophrenic disorder, camnesia or Tourette's disorder. The polynucleotides may be used in chybridisation and amplification technologies, e.g. in assessing gene cexpression patterns, to develop a transcript image for a particular cell cor tissue, or to create transgenic animals to model human disease. This sequence encodes a human secretory protein isolated in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes an isolated polynucleotide a naturally occurring polynucleotide sequence at least 90 % identical to it, a polynucleotide complementary to it or an RNA equivalent of it. The purified secretory polypeptides (SPTM) and polynucleotides are useful in the diagnosis,
Sequence 2311 BP; 824 A; 325 C; 473 G; 689 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 260-261; 340pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 decreased expression of functional secretory molecules, e.g. AIDS, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purified secretory polypeptides and polynucleotides, useful in the gnosis, study, prevention or treatment of diseases associated with
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Liu
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B, Flores V,
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V, Daffo A,
David MH, L
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Chen
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ADT96256/c
ID ADT962
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AC ADT962
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Colon
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                                                                                                                                                                                                                     RESULT
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                 Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; humoral immune response; cellular immune response; cytostatic; immunostimulant; human; ss.
                                                                                                                    16-DEC-2004
                                                                                                                                                   ADT96256;
                                                                                                                                                                                   ADT96256 standard; cDNA; 544
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                                                                                                                                                                                                                                                                                                     671
                                                                                   cancer
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                                                                                                                                                                                                                                                                                                     GACTATCAAATCATACAGATATTGTCAAA 699
                                                                                                                                                                                                                                                                                                                                      CAGCTTAGTTTTCTTACTTTTTAAAATTAATTTGGGTGATGTTTTAATCTAACTTGGACAT
                                                                                                                                                                                                                                                                      TAATCATTTCTCATGTTTATATTTTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                         AGTTTAAACAATTTCCTTAAAATTATTACTAGCTGTTTTTTTGTTTCCTCATCATATTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                 associated human cDNA sequence #1763.
                                                                                                                  (first entry)
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protein.

DNA organisation;

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RESULT 9
AAS29224/c
ID AAS292
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AC AAS292
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                                                                                                                                                                                                                                                                                                                     The invention relates to polynucleotide and polypeptide sequences CC associated with cancer, particularly colon cancer. Also disclosed are (i) CC an expression vector comprising the polynucleotide, (ii) a host cell CC transformed or transfected with the expression vector, (iii) an isolated antibody, or its antigen-binding fragment, which specifically binds to CC the polypeptide, (iv) a method of detecting or determining the presence CC of cancer in a patient, (v) a fusion protein comprising at least one of CC the polypeptides, (vi) an oligonucleotide that hybridises to the polypeptide sequence under highly stringent conditions, and (vii) a CC method of stimulating and/or expanding T cells specific for a tumour CC protein. The polypeptide specifically comprises the amino acid sequence CC of C34S, C637S, C637S, C640S, C636S or one of the potential open reading CC frames (ORFS) of C636S. These polypeptides are encoded by the CC polynucleotide sequences, where both are capable of eliciting a humoral CC and/or cellular immune response. The polynucleotides, polypeptides, and CC antibodies are useful for diagnosing, preventing or treating cancer. CC particularly colon cancer. The polynucleotide and polypeptide sequences are also useful in DNA strand invasion, antisense inhibition, mutational CC analysis, nucleic acid purification, isolation of transcriptionally cative genes, blocking or transcription factor binding, genome cleavage, CC or in situ hybridisation, and as enhancer colon cancer associated CC cDNA. Note: The sequence represents a human colon cancer associated CC construction the USPTO web site at sequents.
                                                                                                                                                                                                                                                      Query Match
Best Local 9
                                                                                                                                                                                                                                        Matches
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Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-2001; 2001US-0267400P.
07-FEB-2001; 2001US-0267382P.
11-MAY-2001; 2001US-0290322P.
12-JUL-2001; 2001US-0313077P.
                 AAS29224;
                                                                                                                                                                                                                                                                                                Sequence 544 BP; 181 A; 70 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acids and polypeptides capable of eliciting humoral and/or cellular immune response, useful for diagnosing, preventing or treating cancer, particularly colon cancer.
                                           AAS29224 standard; DNA; 7736 BP
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                                                                                                                                              601 TCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTT
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                                                                                                                                                                                                                                                        Similarity
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ilarity 57.5%;
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Smith CL,
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L, Durham M,
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Stolk
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    14-AUG-2000

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18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

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05-SEP-2000

06-SEP-2000

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08-SEP-2000

08-SEP-2000
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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19-MAY-2000;
07-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2000;
14-AUG-2000;
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2000US-0225213P
2000US-0225267P
2000US-0225268P
2000US-0225268P
2000US-0225757P
2000US-0225759P
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2000US-0231249P
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2000US-0231249P
2000US-0231296P
2000US-0231296P
2000US-0231296P
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2000US-0216880P.
2000US-0217487P.
2000US-0217496P.
2000US-0218290P.
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2000US-0198123P.
2000US-0205515P.
2000US-0209467P.
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2000US-0224519P.
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2000US-0220964P.
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2000US-0215135P.
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14-SEP-2000
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21-SEP-2000
25-SEP-2000
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29-SEP-2000
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01-NOV-2000
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05-DEC-2000
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05-DEC-2000
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2000US-0233065P
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2000US-0235834P
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2000US-0235836P
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2000US-024921P
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2000US-0232400P.
2000US-0232401P.
2000US-0233063P.
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RESULT 10
ABA16123;
ID ABA16123;
XX ABA16123;
AC ABA16123;
XX ABA16123;
AC ABA16123;
XX Z3-JAN-20;
XX Z3-JAN-10;
XX Human ner
XX Human; no;
KW immunosup;
KW antiparkii

ABA16123;

standard;

DNA;

ΒP

Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;

Human nervous system related polynucleotide SEQ ID NO

8454

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230

TGGTAGCAGCTGTACCA TTGAAGCAACCGCACTA

5048 246 5124

GAAGTACTCCACTCTCCCGAGTCTGCCTTTCCCTCATGGCCTCTGACCTCGCTCCCC

5065

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5125 169

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                                                                                                                                                                                                                                                                                                                      The present invention relates to the isolation of novel DNA-binding CC proteins (AAUJ8154-AAUJ8281), and cDNA and genomic sequences encoding for these proteins. DNA-binding proteins such as histones, chromatin CC organisation modifier) domain proteins, and Y-box binding proteins may CC contribute to diseases resulting from aberrant DNA organisation and/or gene transcription. The sequences of the invention are useful in CC screening assays to identify antagonists and/or agonists that may enhance CC or block activities mediated by DNA-binding proteins. Blockers of DNA-binding proteins may be useful in treating disorders such as malignant CC diseases (e.g. cancer), autoimmune disorders (e.g. diabetes mellitus), rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities CC (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological CC disorders (e.g. Alzheimer's disease). The polymucleotide sequences of the CC invention may also be used in gene therapy. AAS29158-AAS29239 represent CC sequence data for this patent did not form part of the printed CC septence data for this patent did not form part of the printed CC septence of the main of the printed of the printed contents of the printed conte
                                                                                                                                                                               Query Match
Best Local Similarity
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06-DEC-2000;

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08-DEC-2000;

08-DEC-2000;

08-DEC-2000;

08-DEC-2000;

11-DEC-2000;

15-JAN-2001;
                                                                                                                                                                                                                                                         Sequence 7736 BP; 1672 A; 1981 C; 2164 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, Alzheimer's and Parkinson's diseases and cancers.
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                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                               5184 GTTCAGGGGATGGATGTAAAGCACACACAGTTGTTCCCCCCACAGCCGCCCAGATGTG
               170
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GGACCCCTCTCTCCCCGCACGATTTCTTCTTTCATATCTTCCTTTTATTCCTATCCCG
                                                                                              Barash
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2000US-0251479P.

); 2000US-0251868P.

); 2000US-0251869P.

); 2000US-0251989P.

); 2000US-0251999P.

); 2000US-0254097P.

); 2001US-0259678P.
                                                                                                                                                           Conservative
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                                                                                                                                                                          5.2%;
54.7%;
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                                                                                                                                                        Score 37.8; DB Pred. No. 2.9; 0; Mismatches
                                                                                                                                                           0,
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                                                                                                                                                                                                                                                           1919
                                                                                                                                                           62;
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08-SEP-2000; 2000U 08-SEP-2000; 2000U 08-SEP-2000; 2000U 08-SEP-2000; 2000U 12-SEP-2000; 2000U 14-SEP-2000; 2000U	PR 14-AUG-2000; 2000US-022547P. PR 14-AUG-2000; 2000US-022575PP. PR 14-AUG-2000; 2000US-0225759P. PR 14-AUG-2000; 2000US-0225759P. PR 18-AUG-2000; 2000US-0226759P. PR 22-AUG-2000; 2000US-0226686P. PR 22-AUG-2000; 2000US-0227882P. PR 23-AUG-2000; 2000US-0227009P. PR 01-SEP-2000; 2000US-022794P. PR 01-SEP-2000; 2000US-0229343P. PR 01-SEP-2000; 2000US-0229343P. PR 01-SEP-2000; 2000US-0229343P. PR 05-SEP-2000; 2000US-0229343P. PR 05-SEP-2000; 2000US-0239343P. PR 06-SEP-2000; 2000US-0239349P. PR 06-SEP-2000; 2000US-0239349P. PR 06-SEP-2000; 2000US-0239349P. PR 06-SEP-2000; 2000US-0239343P. PR 06-SEP-2000; 2000US-0239343P. PR 06-SEP-2000; 2000US-023943P.	18-APR-2000; 2000U 19-MAY-2000; 2000U 07-JUN-2000; 2000U 07-JUN-2000; 2000U 30-JUN-2000; 2000U 07-JUL-2000; 2000U 11-JUL-2000; 2000U 11-JUL-2000; 2000U 11-JUL-2000; 2000U 14-JUL-2000; 2000U 14-AUG-2000; 2000U	antirheumatic; hepatotropic; cerebroprotec antiallergic; antidiabetic; antiulcer; antiulcer; antiparasitic; cardiant; immune disorder; neurological disease; infection; nephrotro Homo sapiens. WC200159063-A2. 16-AUG-2001. 17-JAN-2000; 2001WO-US001334. 31-JAN-2000; 2000US-0180628P. 24-FEB-2000; 2000US-0184664P. 02-MAR-2000; 2000US-018974P. 17-MAR-2000; 2000US-018974P.
17-NOV- 17-NOV- 17-NOV- 11-DEC- 01-DEC- 05-DEC- 05-DEC- 05-DEC- 06-DEC- 08-DEC- 08-DEC- 08-DEC- 08-DEC- 08-DEC- 08-DEC-	PR 08-NOV-2 PR 08-NOV-2 PR 08-NOV-2 PR 08-NOV-2 PR 17-NOV-2	20-OCT 20-OCT 20-OCT 20-OCT 20-OCT 20-OCT 20-OCT 20-OCT 20-OCT 20-OCT 20-NOV 08-NOV 08-NOV 08-NOV 08-NOV 08-NOV 08-NOV	### 11-SEP ### 11-SEP ### antifungal; ### 21-SEP ### artifungal; ### 21-SEP ### 25-SEP ### 25-SEP ### 27-SEP ### 27-SEP ### 27-SEP ### 27-SEP ### 29-SEP #
000; 2000US-024929 000; 2000US-024929 000; 2000US-025916 000; 2000US-025116 000; 2000US-025116 000; 2000US-025103 000; 2000US-0251479 000; 2000US-0251856 000; 2000US-0251869 000; 2000US-0251869 000; 2000US-0251869	000; 2000US-024653 000; 2000US-024661 000; 2000US-024661 000; 2000US-024920 000; 2000US-024920 000; 2000US-024920 000; 2000US-024921 000; 2000US-024921	000; 2000US-0241785 000; 2000US-0241785 000; 2000US-0241787 000; 2000US-0241808 000; 2000US-0241826 000; 2000US-02448227 000; 2000US-0244677 000; 2000US-0246477 000; 2000US-0246477 000; 2000US-0246477 000; 2000US-0246478 000; 2000US-0246478 000; 2000US-0246478 000; 2000US-0246478 000; 2000US-0246536	000; 2000US-0234223 000; 2000US-0234274 000; 2000US-0234999 000; 2000US-0235894 000; 2000US-0235834 000; 2000US-0235836 000; 2000US-023636 000; 2000US-023636 000; 2000US-023636 000; 2000US-023636 000; 2000US-023636 000; 2000US-023630 000; 2000US-023630 000; 2000US-0237039 000; 2000US-0237039 000; 2000US-0237039

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diabetes mellitus; allergy; asthma; inflammatory condition; thrombot graft-versus-host disease; blood-related disorder; atherosclerosis; hyperproliferative disorder; cancer; renal disorder; arrhythmia; acute glomerulonephritis; cardiovascular disorder; respiratory disord Goodpasture's syndrome; neurological disorder, Alzheimer's disease; Parkinson's disease; endocrine disorder; Addison's disease; reproductive system disorder; endometriosis; infectious disease; viral infection; bacterial infection; fungal infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                  Human; DNA-binding protein; B cell immunodeficiency; autoimmune disorder; severe combined immunodeficiency; rheumatoid arthritis; Crohn's disease; diabetes mellitus; allergy; asthma; inflammatory condition; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-2002
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11-DEC-2000; 2000US-0254097P
05-JAN-2001; 2001US-0259678P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME
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RUBEN S M
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Novel DNA-binding protein useful for diagnosis, prognosis, treatment of immune, hyperproliferative, respiratory, card reproductive, endocrine, gastrointestinal and neurological

respiratory, cardiovascular, neurological disorders

prevention

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RESULT 12
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ID ADC254
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO or the patent did rectly from USPTO or the patent did rectly from USPTO or the patent did rectronic format directly from USPTO or the patent did rectronic format directly from USPTO or the patent did rectronic format directly from USPTO or the patent did rectronic format directly from USPTO or the patent did rectronic format directly from USPTO or the patent did rectronic format directly from USPTO or the patent did rectronic format directly from USPTO or the patent did rectronic format directly from USPTO or the patent did rectronic format directly from USPTO or the patent did rectronic format directly from USPTO or the patent did rectronic format directly from USPTO or the patent did rectronic format di
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Best Local
                                                                                                                                                                                                                                                                                   respiratory-Gen; immunosuppressive; cerebroprotective; vasotropic; nootropic; antiallergic; cancer; bacterial infection; viral infection; neural disorder; immune system disorder; blood disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                               Extracellular matrix protein; cytostatic; antibacterial; virucide neuroprotective; gynaecological; gastrointestinal-Gen; cardiant; cardiovascular-Gen; nephrotropic; antiinflammatory; muscular-Gen;
                                                                                                                                                                                                                                                          pulmonary dis inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA from extracellular matrix gene 78 #3.
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  31-JAN-2000; 2000US-0179065P
                                              07-MAR-2002; 2002US-00091483
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                                                                                               13-MAR-2003.
                                                                                                                                              US2003049650-A1
                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                             disorder;
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                                                                                                                                                                                                                                                             proliferative
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Pred. No. 2.9;
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New DNA-binding treating and/or
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DB; ADC25241.
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                                                                                          HUMAN
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2000US-0251868P.
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                                                                                        GENOME
proteins and gene encoding them, useful for diagnosing, preventing e.g. neurological, inflammatory, infectious,
                                                                  , MS
                                                                                          SCI
                                                                   Barash
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Matches
                                                                                                                                                                      Homo
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cc novel genes. Also included are recombinant vectors, host cells

(c expressing the protein, the extracellular matrix proteins (including

their fragments, epitopes and homologues), an isolated antibody that

cc binds specifically to the protein, diagnosing a pathological condition or

susceptibility to a pathological condition (comprising determining the

cc presence or absence of a mutation in the nucleic acid and diagnosing a

cc condition based on the presence or absence of the mutation), diagnosing a

cc condition based on the presence or amount of expression of the

cc comprising determining the presence or amount of expression of the

cc protein in a biological sample and diagnosing a condition based on the

cc presence or amount of expression of the protein), preventing, treating or

cc ameliorating a medical condition of the protein to a mammalian subject, identifying a binding partner to the

cc protein to a mammalian subject, identifying a binding partner to the

cc protein, the gene corresponding to the cDNA sequence, and identifying an

activity in a biological assay (comprising expressing the nucleic acid in

calculation the emperature of the protein of the protein of the protein and identifying an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a cell, isolating the supernatant, detecting an activity in a biological assay and identifying the protein in the supernatant having the activity). The nucleic acids and proteins display the following activities Cytostatic, antibacterial, Virucide, Neuroprotective,
                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                        20-FEB-2001; 2001WO-US005171.
                                                                                                                                                                                                        23-AUG-2001
                                                                                                                                                                                                                                              WO200160860-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGTACTCCACTCTCCCGAGTCTGCCTTTCCCTCATGGCCTCTGACCTCGCTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGTAGCAGCTGTACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGAAGCAACCGCACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ion relates to an isolated nucleic acid molecule (cDNA) human extracellular matrix protein, representing one os. Also included are recombinant vectors, host cells
                      ; 2000US-0183319P.
; 2000US-0189862P.
; 2000US-0207454P.
; 2000US-0211314P.
; 2000US-0219007P.
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54.7%;
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Pred. No. 2.9;
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MILLENNIUM

PREDICTIVE MEDICINE

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RESULT 14
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Best Local (
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31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is affilicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                               Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; antionvulsant; antibacterial; antifungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schlegel R,
                                                                                                                                                                                                                                         musculoskeletal
                                                                                                                                                                                                                                                  cardiant; gene therapy; cancer; immune disorder; neurological disease; infection; human; secreted
                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                            08-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                     AAL35477;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 386
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                                                                                                                                  17-JAN-2001;
                                                                                                                                                            02-AUG-2001
                                                                                                                                                                                      WO200155367-A1
                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates
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                                                                                                                                                                                                                                                                                                                                 musculoskeletal system related polynucleotide SEQ ID
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2000US-0179065P.
2000US-0184664P.
2000US-0184664P.
2000US-0186350P.
2000US-0189874P.
2000US-0199123P.
2000US-0198123P.
2000US-0209467P.
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                                                                                                                                                                                                                                         system;
                                                                                                                                                                                                                                                                                                                                                                                                               cDNA;
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11-NO
(ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins
                                                                                                                        Claim
                                                                                                                                                                       disorders
                                                                                                                                                                                                                            2001-451937/48.
DB; ABB03895.
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                                                                                                                                                d polypeptide for treating, preventing and/ or prognosing rs related to the musculoskeletal system including musculoskeletal and also for testing and detection e.g. diagnosis.
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04-FEB-2000;
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07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 periodontal regeneration; tissue transport; bone graft; skin aging; keratinocyte growth; hair loss; melanocyte growth; cell proliferation; cell growth; organ transplant; cell differentiation; body height; weight; hair colour; sye colour; skin; percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism; biorhythm; caricadic rhythm; depression; tendency for violence; pain; reproductive capability; hormone level; endocrine level; appetite; libido; memory; stress; storage capability; fat content; lipid content; protein content; carbohydrate content; vitamin content; cofactor content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          post-operative tissue repair; limb regeneration; neuronal growth; neurodegenerative disorder; Alzheimer's disease; Parkinson's dise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene; ss; musculoskeletal system antigen; cancer; metastasis;
re-vascularisation; thrombosis; arteriosclerosis; mineral content;
cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
                                                                                                                                                                                             17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      nutritional
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                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding novel human musculoskeletal system antigen #809.
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       The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and limb regenerative tissue repair, and ulcers; stimulates angiogenesis and limb regenerative incurrant disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or
                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.
                                                                                                                                                                                         Claim 1; SEQ
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skin aging

due to sunburn by stimulating

in animals or

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CC activate hair-forming cells and promotes melanocyte growth; stimulates
CC growth and differentiation of hematopoietic cells and bone marrow cells
CC when used in combination with other cytokines; maintains organs before
CC induces tissue of mesodermal origin to differentiate in early embryos;
CC increases or decreases the differentiation or proliferation of embryonic
CC stem cells, besides, haematopoietic lineage; modulates mammalian
CC characteristics, such as, body height, weight, hair colour, eye colour,
CC skin, percentage of adipose tissue, pigmentation, size, and shape (e.g.,
CC cosmetic surgery); modulates mammalian metabolism; changes mammal s metal
CC depression, tendency for violence, tolerance for pain, reproductive
CC capabilities, hormonal or endocrine levels, appetite, libido, memory, or
CC stress; increases or decreases storage capabilities, fat content, lipid,
CC omponents. This sequence encodes a novel human musculoskeletal system
CC printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                        Sequence 366 BP; 120 A; 59 C; 53 G; 133 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                 printed specification, but wa
from the US patent office at
                                                                                                                                                                                                                                                                                                                                                              ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140
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Pred. No. 1
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Search completed: August 27, 2005, 08:07:49 Job time : 534 secs

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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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SUMMARIES
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Result No.	Score	Query	Query Match Length DB ID	8	ID	Description
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ALIGNMENTS

RESULT 1 US-10-776-213-2

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Sequence 2, Application US/10776213

Publication No. US20040142478A1

GENERAL INFORMATION:
APPLICANT: ASTRIAGENERA AB

TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for Controlling Nucle
TITLE OF INVENTION: Acid Expression
FILE REFERENCE: 3526,82543

CURRENT APPLICATION NUMBER: US/10/776,213

CURRENT APPLICATION NUMBER: US/10/776,213

CURRENT FILING DATE: 2004-02-12

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 723

TYPE: DNA

ORGANISM: Saccharomyces cerevisiae

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  ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAT 120
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RESULT 2
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; Sequence 24, Application US/10776213
; Publication No. US20040142478A1
; GENERAL INFORMATION:
APPLICANT: AstraZeneca AB
; TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for Controlling Nucl
; IITLE OF INVENTION: Acid Expression
; FILE REFERENCS: 3526.82543
; CURRENT APPLICATION NUMBER: US/10/776,213
; CURRENT FILING DATE: 2004-02-12
; NUMBER OF SEQ ID NOS: 32
coptware: Patentin Ver. 2.0
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                                                                                           ; TYPE: DNA ; ORGANISM: Saccharomyces cerevisiae US-10-776-213-24
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                                                  Score 723; DB 19;
Pred. No. 4.7e-216;
D; Mismatches 0;
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Sequence 20, Application US/10776213

Publication No. US20040142478A1

GENERAL INFORMATION:
APPLICANT: AstraZeneca AB

TITLE OF INVENTION: Compositions and Methods Utilizing Seq
TITLE OF INVENTION: Acid Expression
FILE REFERENCE: 3526.82543

CURRENT APPLICATION NUMBER: US/10/776,213

CURRENT FILING DATE: 2004-02-12

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 20
LENGTH: 13073
               Query Match
Best Local Similarity
Matches 723; Conserva
                                                                                                ; TYPE: DNA ; ORGANISM: Saccharomyces cerevisiae US-10-776-213-20
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US-10-776-213-20
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                             100.0%; Score 723; DB 19; ilarity 100.0%; Pred. No. 5.1e-216; Conservative 0; Mismatches 0;
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RESULT 4
US-10-776-213-30
; Sequence 30, Application US/10776213
; Publication No. US20040142478A1
; GENERAL INFORMATION:
; APPLICANT: AstraZeneca AB
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                             ; TYPE: DNA ; ORGANISM: Saccharomyces cerevisiae US-10-776-213-30
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                                                       TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for Controlling Nucl
TITLE OF INVENTION: Acid Expression
FILE REFERENCE: 3526.82543
CURRENT APPLICATION NUMBER: US/10/776,213
CURRENT FILING DATE: 2004-02-12
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 850
Query Match
Best Local Similarity
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 99.6%;
Score 720.4; DB 19;
Pred. No. 7.6e-216;
           Length 850;
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US-10-451-467A-317
US-10-451-467A-317
; Sequence 317, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
APPLICANT: CONTRERAS, ROLAND HENRI
APPLICANT: EBERHARDT, INES
APPLICANT: EBERHARDT, INES
APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRU
TITLE OF INVENTION: VEAST AND FUNGI
FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: EP 00870318.3
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-01-04
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GENERAL INFORMATION:
APPLICANT: Baker Kevin P
APPLICANT: Beresini, Mau:
APPLICANT: DeForge, Laur:
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ell;
APPLICANT: Goo, Wei-Qian;
APPLICANT: Gerritsen, Mai
APPLICANT: Goddard, Audri
                                                                                                                                                                                                                                                                                       RESULT 6
US-10-123-155-198/c
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                                                                                                                                                                                                                                                            Sequence 198, Application US/10123155 Publication No. US20030068794A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: EP 01870003.
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 317
LENGTH: 680
                                                    APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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Best Local Similarity
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APPLICANT
                         APPLICANT:
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                                                                                               Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                                    Smith, Victoria
Stewart, Timothy A.
                                                                                                                                                                      Desnoyers, Luc
Filvaroff, Ellen
          Watanabe, Colin K
Wood, William
                                     Tumas, Daniel
                                                                                Sherwood, Steven
                                                                                                                                           Gerritsen, Mary E
                                                                                                                                                          Gao, Wei-Qiang
                                                                                                                                                                                                   DeForge, Laura
                                                                                                                                                                                                                   Beresini, Maureen
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Pred. No. 1.2e-145;
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CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 5.7%; Score 41;
Similarity 7.7%; Pred. No. 0.
                                                            DM.S.M.ATMR...H 280
                                                                                                                         .YBBBCSMAAA.YRA.NG.TWT.RRASK..A.S.DHABWCH...BSA.B.KNS.S.RAT.
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                                                                                                                                                                                                                                                                                                             ..TTCMMRT.WH.BYH.HAT..B..SB.DSST.CH..KB.D.BHA..Y.M.KNWC.R.RH
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                                                                                           AAGACTAATAATAAC
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Sequence 198, Application US/10146731 Publication No. US20030129692A1 GENERAL INFORMATION:

APPLICANT: Baker, Kevin APPLICANT: Beresini, Ma

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SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C323
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT FILING DATE: 2002-05-15
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                                                                  GAGTTGTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGG
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                                                                                                  ACB...RDT.C.M.WBH.WWB.AB.HC.W.DG..DB.BKABH..RS.SSBS.H...Y..B
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C168
CURRENT FILING DATE: 2002-05-06
CURRENT FILING DATE: 2002-05-06
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
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Best Local Similarity
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                        52; Conservative 194; Mismatches 429;
               GCGCCCGTTTCCCAATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCTTCCTATTTG 466
                                                 SBDSYNCBB.A...W.RSNN..M.TMAMTS.HR..D..A...YN.TAANC..A.B.RCK 595
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                                                                              GAACAGGGGCTACAGTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCG 406
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                                                                                                                                                   GTGTATCTCACAGTGGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTA 346
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Wood, William
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Gerritsen, Mary E.
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Gurney, Austin L.
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US-10-141-761-198
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US-10-141-761-198/c
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C198
CURRENT FILING NUMBER: US/10/141,761
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
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ST. DGDMNC.SGT.K.B.YY...D.RST.B.SCN.NNM.WC.M.RAATB.M..R.N..N
                              CCGGGACCCCTCCTCCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATC 226
                                                                GA.T...MM.SBTAASD.MKW...WBH.H..SBCAGRB.HYBN...YNYNSS.WHS..A 835
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                                                                                                Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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                                                                                                                                                                                           5.7%; Score 41; DB ilarity 7.7%; Pred. No. 0.1; Conservative 194; Mismatches
                                                                                                                                                                                                                             DB 15; Length 1024;
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                                                                            Prior Apploication removed - See File Wrapper NUMBER OF SEQ ID NOS: 550 SEQ ID NO 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
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APPLICANT:
                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C248
CURRENT APPLICATION NUMBER: US/10/142,885
CURRENT FILING DATE: 2002-05-10
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                                   TYPE: PRT
ORGANISM: Homo
                                                              LENGTH: 1024
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Wood, William
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Stewart, Timothy A.
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Godowski, Paul J.
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Sequence 198, Application US/10158790
Publication No. US20030180879A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desonyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goodard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Smith, Victoria
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APPLICANT:
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Stewart, Timothy A. Tumas, Daniel
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RESULT 12 US-10-137-871-198/c

Sequence 198, Application US/10137871 Publication No. US20030207350A1 GENERAL INFORMATION:

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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLITILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C448
CURRENT APPLICATION NUMBER: US/10/158,790
CURRENT FILING DATE: 2002-05-30
Prior Application removed - See File Wrapper or Parameter of SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
ORGANISM: Homo Sapien
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US-10-137-871-198
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CURRENT APPLICATION NUMBER: US/10/137,871
CURRENT FILING DATE: 2002-05-03
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K
Wood, William
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DeForge, Laura
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RESULT 13
US-10-140-923-198/c
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
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TYPE: PRT
ORGANISM: Homo S
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CURRENT FILING DATE: 2002-05-07
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TITLE OP INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OP INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C188
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SBDSYNCBB.A...W.RSNN..M.TMAMTS.HR..D..A...YN.TAANC..A.B.RCK
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Gurney, Austin L.
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Filvaroff, Ellen
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APPLICANT: Beresini, Maure,
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Elle
                                                                                                                                                    Query Match
Best Local Similarity
Matches 52; Conserv
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 198, Application US/10141756 Publication No. US20030207359A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-05-08
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C200
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TYPE: PRT
ORGANISM: Homo Sapien
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                               894 GA.T...MM.SBTAASD.MKW...WBH.H..SBCAGRB.HYBN...YNYNSS.WHS..A 835
                                                                                         954 T.CRYAN..MWMHY..MWT.HYCD.NYTBD..BH.TH.H.BB.SN.S.N..YN..NYHHS
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                                                                                                                     ..TTCM/MRT.WH.BYH.HAT..B..SB.DSST.CH..KB.D.BHA..Y.M.KNWC.R.RH
                                                            GAGTTGTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGG
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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                                                                                                                                              5.7%; Score 41; DB 17; I larity 7.7%; Pred. No. 0.1; Conservative 194; Mismatches 429;
                                                                                                                                                                  Score 41; DB 17; Length 1024; pred. No. 0.1;
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Prior Apploication removed - See File Wrapper or NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
ORGANISM: Homo Sapien
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                                                                                       APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93330R1C197
CURRENT APPLICATION NUMBER: US/10/141,759
CURRENT FILING DATE: 2002-05-08
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Gurney, Austin L.
Sherwood, Steven
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774 RN.KYH..MH..R.TYSTTDW...HM..S.RY.....N...RCTYT.S.THH..CTYNS 715
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YBBBCSMAAA.YRA.NG.TWT.RRASK..A.S.DHABWCH...BSA.B.KNS.S.RAT. 295
                                                                         GAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGG
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294 DM.S.M.ATMR...H 280
                                                            354 YBBBCSMAAA YRA.NG.TWT.RRASK..A.S.DHABWCH...BSA.B.KNS.S.RAT. 295
                                                                                                                    14 ..S.CWN.KTTR.DM.BT..H.M..SR.BM.RH.R...YVA.D.TRHCSCYY.TH.YTR
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                              AAGACTAATAATAAC 721
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Search completed: August 27, 2005, 11:43:49 Job time: 658 secs

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Match
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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	Sequence 8463, Ap	Sequence 13969, A	Sequence 16934, A	Sequence 11750, A	Sequence 17576, A	Sequence 17009, A	Sequence 60957, A	Sequence 28524, A	Sequence 12777, A	Sequence 14033, A	Sequence 12373, A	Sequence 14043, A	Sequence 125, App	Sequence 12509, A	Sequence 13212, A	Sequence 13211, A	Sequence 12508, A	Sequence 27, Appl

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Sequence 2, Application US/09743194

Sequence 2, Application US/09743194

Patent No. 6716601

Patent No. 6716601

APPLICANT: Belfield, Graham

APPLICANT: Oakley, Caroline

TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for TITLE OF INVENTION: CONTROLLING Nucleic Acid Expression in Yeast FILE REFERENCE: 3526.82543

CURRENT APPLICATION NUMBER: US/09/743,194

CURRENT FILING DATE: 2001-01-08

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 723

TYPE: DNA

ORGANISM: Saccharomyces cerevisiae

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Length 723;

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Best Local Similarity 100.0%; Pred. No. 1.9e-229;
Matches 723; Conservative 0; Mismatches 0;
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GTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCGGCGCCCCGTTTCCCA
                                      GGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACA 360
                                                                GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTATCTCACAGT
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; ORGANISM: Saccharomyces cerevisiae
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APPLICANT: Oakley, Caroline
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
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GGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACA
                                                                                                                                                                         CTCCCCGCACGATTTCTTCCTTTCATATCTTTCCTTTTATTCCTATCCCGTTGAAGCAACC
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                                                             GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTATCTCACAGT
                                                                                         GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTTGTGTGTATCTCACAGT
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; TYPE: DNA
; ORGANIEM: Saccharomyces cerevisiae
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APPLICANT: Oakley, Caroline
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
TITLE OF INVENTION: Controlling Nucleic Acid Expression in Yeast
TITLE OF INVENTION: Controlling Nucleic Acid Expression in Yeast
TITLE OF INVENTION: Controlling Nucleic Acid Expression in Yeast
TITLE OF INVENTION: CONTROLLING NEW OF SEQ. 10 NO SEQ. 10 NO SEQ. 10 NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ. ID NO 20
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Patent No. 6716601
GENERAL INFORMATION:
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Best Local
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APPLICANT: Oakley, Caroline

APPLICANT: Oakley, Caroline

ITILE OF INVENTION: Compositions and Methods Utilizing Sequences for TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for ITILE OF INVENTION: Controlling Nucleic Acid Expression in Yeast

FILE REFERENCE: 3526.82543

CURRENT APPLICATION NUMBER: US/09/743,194

CURRENT FILING DATE: 2001-01-08

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 30

LENGTH: 850

TYPE: DAN:

OGGANISM: Saccharomyces cerevisiae

US-09-743-194-30
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Patent No. 6716601
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            Query Match 99.6%;
Best Local Similarity 99.9%;
Matches 721; Conservative
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Pred. No. 1.5e-228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08232463
PATENT NO. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF STATES OF THE PROPERTY OF THE PROPER
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNBY/AGENT INFORMATION:
NAME: BERT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
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US-09-949-016-17445
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                                                                                                     PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION UNMEER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
                                                                   SOFTWARE: FastSEQ for Windows Version SEQ ID NO 17445
                                                                                                                                                                                                                                                                                                                                                                    Sequence 17445, Ap
Patent No. 6812339
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Matches 11; Conservative 2
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INFORMATION FOR SEQ ID NO:
                                  LENGTH: 4989
TYPE: DNA
               ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 30-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 0.00024;
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PRIOR PLICATION NUMBER: 60/237,768
PRIOR REILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FBECSEQ for Windows Version 4.0
SEQ ID NO 17442
LENGTH: 11440
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; ORGANISM: Human
US-09-949-016-17442
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                                                     RESULT 8
US-09-949-016-16850/c
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Best Local S
Matches 75
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                     Sequence 16850, Application US/09949016 Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                       8713 GAAGTACTCCACTCTCCCGAGTCTGCCTTTCCCTCATGGCCTCTGACCTCGCTCCCC 8654
                                                                                                                                                                                                                                                                                  8773 GTTCAGGGGATGGATGTAAAGCACACACAGTTGTTCCCCCCACAGCCGCCCAGATGTG
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                                                                                                                                TGGTAGCAGCTGTACCA 8637
                                                                                                                                                                  TTGAAGCAACCGCACTA 246
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                        Score 37.8; DB 
Pred. No. 0.36;
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768

ASSOCIATED
OF DETECTION AND USES THEREOF

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US-09-949-016-16850
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SOFTWARE: FBBESEQ for Windows Version 4.0
SEQ ID NO 16850
LENGTH: 16662
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 15
                                                                                                                           Query Match
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                                                                                                 Matches
                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: 44 Human Secreted Proteins FILE REFERENCE: PZ024P1 CURRENT APPLICATION NUMBER: US/09/369,247 CURRENT FILING DATE: 1999-08-05 EARLIER APPLICATION NUMBER: 60/074,118 EARLIER FILING DATE: 1998-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/074,341
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 60/074,157
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,137
EARLIER FILING DATE: 1998-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 172
                                                                                                                                                                                                                                       NAME/KEY: SITE LOCATION: (406) OTHER INFORMATION:
                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (794)
OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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Local Similarity 54.0%;
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594 TTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCT
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                              TATCCTGTTATTTAAATGTGAACATTTATTGTACATTCAGTGAGTTATAGTGTTAATAGT
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Pred. No. 1.1;
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US-09-949-016-16144
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 16144
LENGTH: 191433
                                                                                                                                          SEQ ID NO 15419
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Best Local :
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                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                      TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
NAME/KEY: misc_feature
LOCATION: (1)...(212449)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Human
                                                                                                                     SENGTH: 212449
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o. 6812339
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Pred. No. 12;
0; Mismatches 41;
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OF DETECTION AND USES THEREOF
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RESULT 13
US-09-949-016-14133/c
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                                                                                                                                            GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CLOO1307
CURRENT APPLICATION UNMEER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                            Sequence 14133, Application US/09949016 Patent No. 6812339
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LENGTH: 72992
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               PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCCGGGACCCCCTCCTCT
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Pred. No. 13;
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; LENGTH: 102884
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(102884)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17100
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17100
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(98962)
OTHER INFORMATION: n = A,T,C
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Similarity 53.7%;
                                     CATATCTTCCTTTT 217
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Pred. No. 13;
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Pred. No. 13;
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Sequence 26160, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: 05/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEG ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

TYPE: DNA

ORGANISM: Human

US-09-949-016-26160
Search completed: August 27, 2005, 10:04:45 Job time : 182 secs
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                                                                                               289 CATT 286
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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AR492027
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AR492027 Sequence
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Z48639 S.cerevisia
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Gaps 0;	0;	Length 723;; Indels	DB 6; .8e-207;	/ Match 100.0%; Score 723; DB 6; Local Similarity 100.0%; Pred. No. 3.8e-207; nes 723; Conservative 0; Mismatches 0;	Query Match Best Local Matches 72	
,	promoter	ast 2501	the year	Unknown. Unknown. Unclassified. 1 (bases 1 to 723) 1 (formulation of the yeast ZE01 promoter Compositions and methods utilizing the yeast ZE01 promoter Location/Qualifiers 1 (723) 1 (723) /organism="unknown" /mol_type="genomic DNA"	SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES BOUICE ORIGIN	
15-MAY-2004	PAT 15	linear	DNA	AR492027 Sequence 2 from patent US 6716601. AR492027 AR492027.1 GI:47260496	AR492027 LOCUS DEFINITION ACCESSION VERSION	

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Similarity 100.0%; Pred. No. 6.1e-207;
23; Conservative 0; Mismatches 0;
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                                                                      GGGGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCCGGACCCCGGGACCCCTCCT
                                                                                                                              ACCATAAAGAGCAAAGCGATACCTACTTGGAAAGGAAAAGGAGCACGCTTGTAAGGGGGAT
CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTATTCCTATCCCGTTGAAGCAACC
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AUTHORS
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FEATURES
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SOURCE
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Sequence 20
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1 (bases 1 to 13073)

Belfield,G.P. and Oakley,C.

Compositions and methods utilizing the patent: US 6716601-A 20 06-APR-2004;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       Unclassified.
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 GGGGGCTAAGAAGTCATTCACTTTCCTTTCCCTTCGGGGTCCGGACCCGGGACCCCTCCT
                                                                   ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAAGGAGCACGCTTGTAAGGGGGAT
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/mol_type="genomic
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674 660 614 600 554 540 494 480 434 420 374 360 314 300

120 75 60

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61 ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGGAT 120	1 CTTTCGATTAGCACGCACACACACATAGACTGCGTCATAAAAATACACTACGGAAAA 60 	/ Match 99.6%; Score 720.4; DB 6; Length 850; Local Similarity 99.9%; Pred. No. 2.4e-206; nes 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	/mc /mc	Compositions and methods utilizing the yeast ZEO1 promoter Patent: US 6716601-A 30 06-APR-2004; Location Qualifiers 1 1850	-	AR492055.1 GI:47260524	AR492055		721 CAT 723 736 CAT 738	661 TATTGCAGAGGACTATCAAATCATACAGATATTGTCAAAAAAAA	601 TCATATAAAAGGAAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTT 660	541 TTTCGATGAGAGAATTAGCAAGCGGAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAA 600	481 TGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTGATAAGGGATGTAAC 540	421 ATAGGAAGCGCAGTTTATCGGCGAAGCTCTACTTCTTCCTATTTGGGTAAGCCCCTTTC 480	361 GTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCGGCGGCCGCCGTTTCCCA 420	301 GGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACA 360 	241 GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTG	181 CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTATTCCTATCCCGTTGAAGCAACC 240	136 GGGGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCCGGGACCCCTCCT 195
	COMMENT	AUTHORS TITLE JOURNAL	REFERENCE AUTHORS JOURNAL	SOURCE	DEFINITION ACCESSION VERSION KEYWORDS	RESULT SC9920 LOCUS	Db	9	Qy	Qy Db	Qy	AS AG	β δ	qq VQ	Qy ДЪ	dg VQ	Qy da	Db Qy	ф
	ENT	AUTHORS TITLE JOURNAL	FERENCE AUTHORS JOURNAL	URCE ORGANISM	SION SION STON	υ	7	72	66 73	0 0	о 0	4. D		w ea	ωω	ω 2	181 258	121 GGGGGCTAAGAAGTCATTCACTTTCTCTTTTCCCTTCGCGGTCCGGACCCGGGACCCCTCCT	138 ACCATAAAGAGCAAAGCGATACCTACTTGGAAAGGAAAAGGAGCACGCTTGTAAGGGGGAT

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FEATURES
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Cosmid 9920 is overlapped at the start of this sequence by cosmid
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GVEPPDKWEREI EDYFTSDED INSI KVSFEKNLFALLVTSPNESA I SLLEDEFVQLI
ETDESNVENKKOGVYDALNYELDSDMI FLNGKI GKFINEI PTLVOESTYQNFAGIMAO
YSNSKEFKANTDA I TSLEDFFIVAL SENLEKTI I LATMELDADI YQQLMKSDSIELE
LY I EDEMKNYKEDDSGEI FKGNNKFLNGRTI TI TLYRSAVANGVEGFCAVLSKLDETF
FSTLLLNTDEJSCAL KEVSEDTWEKLFULSCLAKGNSEI ANKLAQVI LOHAQVYFSE
GAKEKYVTHAVELI NGCNDTSQI FFFANA I EVFARYMPA I DYRSSLVSSLSTNTHLLL
                       complement (4197.
                                                                                                                                                                                                       small spliced gene"
                                                                                                                                                                                                                                                    complement(join(4101. .4196,4434. .4 /note="YM9920.03c, unknown, len: 55,
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complement(3379. .3706)
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/note="PS00061 Short-chain alcohol dehydrogenase family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDDKFINLKNMQKLIRYALFLDALLDALPERVNNHIVAFITVVSELVTDYNCLSEEPN
DLYYDFGHTFFKHGKVNLNFSDIVGNVIQPANGGDAMLTFDIAESNSVYFFYYSRVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDPAKINALMAVFQEQLLNIVKEIVVNENEDTISDERYSSKEESEFRYHRVIASAVLL
LIKLFVHNKDVSERNSSSLKVILSDESIWKLLNLKNGQNTNAYETVLRLIDVLYTRGY
MPSHKNIMKLAVKKLLKSLTHITSKNILKVCPVLPSILNLLATLDDYEDGTIWSYDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="msfggintfqqyntdlglghngvrislnyfdglpdpsllnslys
NELKLIFKSLLKRDETTKEKALMDLSNLISDFNQNEYFFNDIFLLCWSqiyaKLIISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="YM9920.01c, unknown, PS00061 Short-chain alcohol
                                                     ALAHLCAIYTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKEKVLKFLSVSRTSPSPGFFNAVFALYSSTKRHSFLDYYLEWLPFWQKSVQRLNEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YKVIRLQSHQITIMLVKSLRKKISKFLKDFIPLILLGTCELDYSVSKPSLNELTECFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA88574.1"
/db_xref="GI:732925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (<1. .2870)
                                                                                               /protein_id="CAA88576.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="delta element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="UniProt/Swiss-Prot:004781"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="cosmid 9920"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="13R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:4932"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="AB972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end of this sequence by cosmid 8156.
                                                                          translation="MELMASCFRMPRYRHANDTLGWLLIGLRRLLPLNNKAIIPLNSL
                                                                                                                                                                                                                                                                                                                                   translation="MGELAPMNKPDEGITNMCQSLYRYQIMRMSIGLRRLLPLNNKAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome="XIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Saccharomyces"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type="genomic DNA"
splice acceptor sequence,
                          .4199)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .4196,4691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                len: 61, CAI: 0.17, possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               partial, len:
dehydrogenase
                                                                                                                                                                                                                                                                                 .4505))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .4780))
                                                                                                                                                                                                                                                         CAI: 0.13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            956,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAI:
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                                                                                                                                                                                                                                                                                                              codon_start=1
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/translation="milhrigskoknfeniagkvyhdlaglollsndvoksavosghog hansisteniagkoksavosghog hansistenia
                                                                                                                                                                                                                                                                                          RAFSFELLNSSKLPGCFEIVSSIHESIENDSAPKSVKDYWEHPQAYKPGVPLVAFKLS
KKFHEEYPEVPQAILSSLLRGRGWIIPNYPLPKATDGSDEKEVLRVVFRSEMKLDLAQ
LLIVDIESILTKLIHSYEKVCHHIELASEQTPERKSSFIYEMLLALASPQDDIPTPDE
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7746. .8846
/note="YM9920.05, unknown, len: 366, CAI: 0.11, similar to
YK56_YEAST P36156, YKR076W, hypothetical protein in SIS2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (4428.
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/note="possible splice branch sequence,
                                                                                                                                                                                                                     EKKNKLKETTTRNYRGTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="SGD:S0004862"
db_xref="UniProt/Swiss-Prot:Q04792"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="GOA:Q04792"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein_id="CAA88577.1"
db_xref="GI:732928"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene"
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9519 660 9459

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Query Match
Best Local Similarity
Matches 721; Conserv
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TTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAA
                                                                         TGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTGATAAGGGATGTAAC
                                                                                                                                                                                                        GGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACA
                                                                                                                                                                                                                                                                                                                          GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTATCTCACAGT
                                                                                                                                                                                                                                                                                                                                           CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATCCCGTTGAAGCAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTCGATTAGCACGCACACACATCACATAGACTGCGTCATAAAAATACACTACGGAAAA
                                                                                                                     ATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCTTCCTATTTGGGTAAGCCCCTTTC
                                                                                                                                                  ATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCTTCCTATTTGGGTAAGCCCCTTTC
                                                                                                                                                                                                                                                       GGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA88582.1"
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/note="YM9920.08c, unknown,
questionable orf"
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coiled-coil domain"
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TPIIDDEENSIPLTEFDLSDSK"
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Pred. No. 4.2e-206;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        len: 188,
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contreras,R.H., Eberhardt,I., Luyten,W.H. and Reekmans, Bax-responsive genes for drug target identification in
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   TGGGACGTCTTAACTTTATTGCAGAGGACTATCAAATCATACAGATATTGTCAAAAAAA
                                                                       TGGGAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTC
                                                                                                                        GTGATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGC
                                                                                                                                        GTGATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGC
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                                                      TGGGAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTC
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PHARMACEUTICA N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Saccharomyces cerevisiae"
/mol_type="unassigned DNA"
/db_xref="taxon:4932"
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1 (bases 1 to Gardner, M.J.,
           Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 257757)
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Plasmodium falciparum
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1 (bases 1 to 7218)

Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.

Recombinant fowlpox virus

Patent: US 5670367-A 14 23-SEP-1997;
                                                                                  AE014837.1
                                                                                            complete sequence. AE014837 AE014186
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14 from patent US 5670367.
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Hall, N., Fung, E.,
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 Berriman, M., Hyman, R.W.,
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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complement(<2647....4074)
/locus tag="PF11 0071"
complement(2647....4074)</pre>
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ENBCLYSLNKAKQINAIITLKSVKGSKTLRLAFKIHSQIARBKIKIGDVIYIETNTG
HVKRLGRCNDYAKEYDIEFDBYVSLÞKGSVHKKKEVVOGISLHDLANANFTVGEDL
ASVLNSYLRÞKKTEITEKLRVEINKTVNKFLESGLAEIIFGVLYIDEAHMLDIECFSY
LNRAIESPLAPTLIMATNRGICTVKGTDNISPHGIPVOLISHLDIAHMLDIECFSY
LNRAIESPLAPTLIMATNRGICTVKGTDNISHGIPVOLISHLOTIATLEGNTIIDIKHIE
ILALRAQTEKINITEEGMNYLAKIGIQSSLRFAMLLLEPSRILATLEGNTIIDIKHIE
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2582. .2650
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vvprlygkhlfvekkoffstlyfvttllmkdvtkihavlvayerrksleffvlgikk
anivilvnkkpkklmepniksisfsitavinskmdetipstkvtlflfisilstkiv"
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/locus_tag="pF11_0070"
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384. .2542
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05. .373
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/chromosome="11"
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/locus_tag="PF11_0072"

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/product="hypothetical protein"

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/protein_id="AAN35661.1"

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NEILKKSENILLERSFSFHKEDITIKPELLKELITQKYRKIFQRHDKDCGSSEIQIII
LTFXIFFJTEHMKKNKKDFACLRGLEFKCVSKRRRLLYVIGRKDREMFEKITSYFNIKK
                                                              /rpt_type=tandem
4922. .4970
                                                                                                                                                                                                                         /locus_tag="PF11_0073"

join(<7800. 9712,9978. .10049,10155. .10162,10204. .>10244)

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/bb_xref="GI:23496000"

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7132. .7156
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4718. .4749
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4159. .4258
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                                                 complete sequence.
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                  BX663508.8 GI:40714027
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complement(join(<10677. .10818,10922. .10993,11120. .11199,
11295. .11397,11559. .12736,12847. .>13503))
/locus_tag="PP11_0074"
complement(join(10677. .10818,10922. .10993,11120. .11199,
11295. .11397,11559. .12736,12847. .13503))
/locus_tag="PP11_0074"
/codon_start=1
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13757. .13788
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12185. .12400
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complement(<10677.</pre>
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10372. .10409
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10060. .10092
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/protein_id="AAN35663.1
/db_xref="GI:23496001"
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clone CH211-144B6 in linkage group
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality dear (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPBE; Information on the WORMPBE database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where
                                                                                                                                                                    648
                                                                                                                                                                                                                                                                                                                                            78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-JAN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 6, 2004 this sequence version replaced gi:37805672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Materman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-144B6 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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1. (bases 1 to 170295)
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  ATACTAATAATA 60401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:7955"
/clone="CH211-144B6"
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57.8%;
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Pred. No. 0.3;
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Homo sapiens BAC clone RP11-107
AC092573 AC015764
AC092573.2 GI:15668NB4
                                                                                                                              Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 60 On Sep 19, 2001 this sequence version replaced gi:14916158
                                                                                                                                                                                                                                                                             Direct Submission
Submitted (19-SEP-2001) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                        Waterston,R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                       4 (bases 1 to 171265) Waterston, R.H.
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Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boyer, E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9847074
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center project name: H_NH0001007
Drafting Center: WIBR
                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
                                                      Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
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                                   Summary Statistics
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence restriction digest. from more than one subclone; and the assembly was confirmed by

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McDherson, Department of Genetics, Washington University, St. Louis
MC. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made donor, as described by Osoegawa, K., Woo woon, P.Y., Zhao, B., F f one male Frengen, E.,

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The clone sequenced to the left is RP11-291G2, 1984 bp overlap; th clone sequenced to the right is RP11-15818. Actual start of this clone is at base position 105122 of RP11-291G2; actual end is at base position 171265 of RP11-107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either Research Genetics, Inc. (http://www.resgen.com) or Pieter de and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Data from AC013461, AC073465, AC011667 finish this clone, AC015764.
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/note="match to EST AW814670
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/note="match to EST BE867724
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}588. .3651
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/note="match to EST
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mol_type="genomic DNA"

'db_xref="taxon:9606"

'chromosome="2"
                                                                                                                  note="match to EST
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4. .2351
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                                                BE867724 (NID:g10316500)'
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                           GCTATAAAAAGGAGAAATTAATCCACACAATCTCACACATTCTGGGAGGAAAAATAAACT
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Note="match to EST N95341 (NID:g1267676) zb68f09.sl"
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(NID:g10153317)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="match to EST BF155794
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Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lieu, C., Locke, K., MacQualdi, P., Marquis, N., Klein, J., McEwann, P., McGunk, A., McKernan, K., McLaughlin, J., Maldrim, J., McCwann, P., McGunk, A., McKernan, K., McLaughlin, J., Maldrim, J., McEwann, P., McGunk, A., McKernan, K., McLaughlin, J., Meldrim, J., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
       Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 21, 2000 this sequence version replaced gi:7321517.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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AC012052
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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2, clone RP11-337F19
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Muzny, D., Arenson, A.D., Adams, C., Brundage, E., Bunac, C., Carvelli, K., Chacko, J., Chen, J., Di, W., Ding, Y., Dugan, S., Durbin, J., Forcum, J., Ganesh, R., Garcia, C., Goodman, M., Gorrell, J.H., Haywood, M., Hernandez, J., Jackson, L., Jin, S., Kampal, R., Karpathy, S., Kovar, C., Leal, B., Li, Y., Lichtarge, O., Liu, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L. Rashid, N.D., Rowland, K., Savage, L., Scherer, S.E., Shen, H.,
                                                                                                                                                                                                                                                                                                         Homo sapiens X GSHB-223P11 (Genome
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (17-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
(bases 1 to 80659)
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Direct Submission
Submitted (11-APR-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 80659)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence similarities were identified using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The repeat regions shown were identified using RepeatMasker by Adrian Smit.
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Direct Submission
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                                                         /rpt_family="MIR"
3679. .3861
                       /rpt_family="MER53"
4687. .4829
                                                                                                                                        /rpt_
1933.
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complement(3587.
                                                                                                                                                                             complement (1641.
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                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                          note="overlaps bases 114570.
                                                                                                                                                                                                                                                                                                                               clone="GSHB-223P11"
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                                                                                                                                                                                                                                                                    function="clone overlap"
                                                                                                                                                                                                                                _family="L2"
       family="MER5B
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repeat_region repeat_region

complement (5319 ..5358)
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complement (5853 ..5898)
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complement (5943 ..6244)
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ement(6621)

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complement (7635. .7690)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33326 GAACATAGTTGTCAAGAGTTCAAACTCCGAGTTCAAAGTTAGCATGTTTTTAGAAAATAA 33267
                                                                                                                                                                                                                                                                                                             697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195932 bp DNA linear HTG 04-APR-2000 Homo sapiens chromosome X clone RP11-12D5 map X, WORKING DRAFT SEQUENCE, 9 unordered pieces.
AC021710
AC021710.4 GI:7408016
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       577 GGCTAGCTGGGAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGA 636
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19592)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome X, clone RP11-12D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.9%;
Similarity 51.0%;
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                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(35042...35071)
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repeat_region repeat_region

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 4, 2000 this sequence version replaced gi:6939568.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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2 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 189137 bases at least Q40
Consensus quality: 199288 bases at least Q30
Consensus quality: 199288 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 195122; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 195932)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                               104625
104725
142394
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                             Location,
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73482: gap of
104624: contig
104724: gap of
142393: contig
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195932: contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188972 GAACATAGTTGTCAAGAGTTCAAACTCCGAGTTCAAAGTTAGCATGTTTTTAGAAAATAA 189031
requests: clonerequest@sanger.ac.uk
On Mar 12, 2001 this sequence version replaced gi:13092292.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                  complete sequence.
AL359542
                                                                Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire. CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                       Human DNA sequence from clone
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 28858)
                                                                                                                                                                                   Homo sapiens
                                                                                                   Direct Submission
                                                                                                                    Heath, P.
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RP6-190D15 on chromosome Xq25-26.1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone RP6-190D15 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP4-537K23 is at 28759 in this set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Group. Further Incomment of the http://www.sanger.ac.uk/HGP/Chrx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      database can be found at
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/note="24 copies 2 mer gt 72% conserved"
|3691. .13842
                                                                                                            /note="AluSg repeat: matches 24.
l2081. .12122
                                                                                                                                                                                         note="Alusx repeat:
                                                                                                                                                                                                                                                 10464. .10518
note="7SK repeat: matches 1.
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/note="AluSg1 repeat: matches 1.
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/note="ilmmb8 repeat: matches 6133. .6171 of consensus
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/note="AluSq repeat: matches 1.
                                                                            note="AluSg repeat: matches 253. .294 of consensus"
                                                                                                                                                                    .1889. .12080
                                                                                                                                                                                                                                                                                                           note="L1MB3 repeat: matches 6035. .6127 of consensus"
                                                                                                                                                                                                                                                                                                                                         note="38 copies 2 mer aa 69% conserved"
.0380. .10462
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mol_type="genomic DNA"

db_xref="taxon:9606"
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/note="LIMA2 repeat: matches 6213.
14610. .14726
                                 note="AluSc repeat: matches 1. .306 of consensus"
                                                                                                       note="AluSx repeat: matches 1. .312 of
                                                                                                                                     note="49 copies 2 mer ag 61% conserved"
                                                                                                                                                                            note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                             note="LIME repeat: matches 5500. .5714 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                            note="MIR repeat: matches 115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MER8 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="TIGGER2 repeat: matches 1. .70 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MER8 repeat: matches 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1MA9 repeat: matches 6110. .6218 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1MB4 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluSg repeat: matches 38. .290 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1MB4 repeat: matches 5639. .5652 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="AluY repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MLT1B repeat: matches 1. .388 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ote="LlP4 repeat: matches 5345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ote="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ote="L1PA12 repeat: matches 5937. .6158 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e="Weakly double-stranded"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="L1MB4 repeat: matches 5646. .6176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .20339
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                                                                                                                          26865
                                                                                                                                                             26067
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                                                                                                                                                                                                                                                                                                                 repeat: matches 5627. .5818 of consensus"
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                                                                  repeat: matches 453.
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525.
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                                                                                                                                                                                                                                                                                                                                                                                            .254 of consensus"
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ORGANISM
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KEYWORDS
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                                                       FEATURES
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                                                                                                                                                                                                           During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP than their source databases are used to associate primary accession the wormPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13671 AC 13670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               710 AC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      590 TTGTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGAC 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 29, 2002 this sequence version replaced gi:21727348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL645468 209764 bp DNA linear ROD 26-JUL-2002 Mouse DNA sequence from clone RP23-246F18 on chromosome 4, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-246F18 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 209764)
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                                                                                 pBACe3.6.
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                                                 Location/Qualifiers
/organism="Mus musculus"
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Pred. No. 0.
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Matches 64; Conserv
                                                                                                                 187 GCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATCC 227
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                                                          TICCCCTTTCCCCTTTCCCTTTTCCTTTCCTTTCC
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                        /clone="RP23-246F18"
/clone_lib="RPCI-23"
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/db_xref="taxon:10090"
/chromosome="4"
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Pred. No. 1.2;
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